

Resource Summary Report

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MEGA

RRID:SCR_000667

Type: Tool

Proper Citation

MEGA (RRID:SCR_000667)

Resource Information

URL: <http://megasoftware.net/>

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Description: Software integrated tool for conducting automatic and manual sequence alignment, inferring phylogenetic trees, mining web based databases, estimating rates of molecular evolution, and testing evolutionary hypotheses. Used for comparative analysis of DNA and protein sequences to infer molecular evolutionary patterns of genes, genomes, and species over time. MEGA version 4 expands on existing facilities for editing DNA sequence data from autosequencers, mining Web-databases, performing automatic and manual sequence alignment, analyzing sequence alignments to estimate evolutionary distances, inferring phylogenetic trees, and testing evolutionary hypotheses. MEGA version 6 enables inference of timetrees, as it implements RelTime method for estimating divergence times for all branching points in phylogeny.

Abbreviations: MEGA, MEGA6, MEGA4, MEGA 4, MEGA 11

Synonyms: MEGA11, Molecular Evolutionary Genetics Analysis, Molecular Evolutionary Genetics Analysis 6, Molecular Evolutionary Genetics Analysis 4

Resource Type: software application, data analysis software, sequence analysis software, software resource, data processing software, software toolkit

Defining Citation: [DOI:10.1093/molbev/msab120](https://doi.org/10.1093/molbev/msab120), [PMID:24132122](https://pubmed.ncbi.nlm.nih.gov/24132122/), [PMID:31904846](https://pubmed.ncbi.nlm.nih.gov/31904846/), [PMID:22923298](https://pubmed.ncbi.nlm.nih.gov/22923298/), [PMID:21546353](https://pubmed.ncbi.nlm.nih.gov/21546353/), [PMID:17488738](https://pubmed.ncbi.nlm.nih.gov/17488738/), [PMID:15260895](https://pubmed.ncbi.nlm.nih.gov/15260895/), [PMID:11751241](https://pubmed.ncbi.nlm.nih.gov/11751241/), [PMID:8019868](https://pubmed.ncbi.nlm.nih.gov/8019868/)

Keywords: comparative, analysis, DNA, protein, sequence, molecular, evolution, pattern, gene, genome, evolution, FASEB list

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NSF ABI 1661218;
NIGMS R35GM139504

Availability: Free, Available for download, Freely available

Resource Name: MEGA

Resource ID: SCR_000667

Alternate IDs: SCR_023017, nlx_156838

Alternate URLs: <https://www.megasoftware.net/mega4/>

Record Creation Time: 20220129T080202+0000

Record Last Update: 20260729T044002+0000

Ratings and Alerts

No rating or validation information has been found for MEGA.

No alerts have been found for MEGA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2763 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Liu J, et al. (2026) FERONIA kinase and PP2A antagonistically regulate salt tolerance in Arabidopsis. Current biology : CB, 36(2), 370.

Edge RJ, et al. (2025) Preclinical evaluation of the neutralising efficacy of three antivenoms against the venoms of the recently taxonomically partitioned *E. ocellatus* and *E. romani*. PLoS neglected tropical diseases, 19(8), e0013371.

Javier MCF, et al. (2025) Draft genome of the endangered visayan spotted deer (*Rusa alfredi*), a Philippine endemic species. GigaByte (Hong Kong, China), 2025, gigabyte150.

José O, et al. (2025) Different populations of mouse egg cortical vesicles are responsible for post-fertilization zinc sparks and proteolysis of the zona pellucida. iScience, 28(6), 112606.

Deézsi-Magyar N, et al. (2025) Evaluating enterovirus diversity among symptomatic patients in Hungary during and after easing the COVID-19 lockdown. Virology journal,

22(1), 204.

Zhuang X, et al. (2025) Rice stripe virus NS3 uses the host signaling pathways to control pathogenicity. *Developmental cell*, 60(17), 2363.

Ito K, et al. (2025) Characterization of the NRPS operon homolog for surfactin A and surfactin C synthesis in *Bacillus* spp. *Archives of microbiology*, 207(7), 161.

Chen PY, et al. (2025) Previously unrecognized diversity of far-red light-using terrestrial green algae and cyanobacteria. *iScience*, 28(10), 113486.

Galvis-Marín JC, et al. (2025) Characterisation of Antifungal Resistance to Azoles in Colombian Isolates of *Malassezia* spp. *Mycoses*, 68(9), e70112.

Wang G, et al. (2025) Genomic evidence for hybridization and introgression between blue peafowl and endangered green peafowl and molecular foundation of leucistic plumage of blue peafowl. *GigaScience*, 14.

Kumar V, et al. (2025) Whole genome sequencing and assembly of the house sparrow, *Passer domesticus*. *GigaByte (Hong Kong, China)*, 2025, gigabyte161.

Mohan HM, et al. (2025) Endogenous retrovirus-like proteins recruit UBQLN2 to stress granules and shape their functional biology. *Science advances*, 11(29), eadu6354.

Xu L, et al. (2025) VCF2Dis: an ultra-fast and efficient tool to calculate pairwise genetic distance and construct population phylogeny from VCF files. *GigaScience*, 14.

Kang YY, et al. (2025) Comparative Effects of Probiotics and Paraprobiotics Derived from *Lactiplantibacillus plantarum*, *Latilactobacillus sakei*, and *Limosilactobacillus reuteri* in a DSS-Induced Ulcerative Colitis Mouse Model. *Journal of microbiology and biotechnology*, 35, e2411045.

Lu Y, et al. (2025) Intrahepatic Microbial Heterogeneity in Multifocal Hepatocellular Carcinoma and Its Association with Host Genomic and Transcriptomic Alterations. *Cancer discovery*, 15(8), 1630.

Shao R, et al. (2025) ZAP inhibits double-stranded RNA virus infection by degrading negative-strand RNA and blocking the elongation phase of viral protein synthesis. *Cell reports*, 45(1), 116742.

Rohan P, et al. (2025) High expression of THY1 is a prognostic marker for gastric Cancer: Deciphering its transcriptional regulation as a component of the Epithelial-mesenchymal transition. *Biochemistry and biophysics reports*, 42, 102050.

Peñaherrera E, et al. (2025) *Desmodium molliculum* (Kunth) DC., an Andean medicinal plant: DNA barcoding and HPLC fingerprint for species discrimination and evaluation of its pharmacological potential. *Frontiers in plant science*, 16, 1612556.

Hathi P, et al. (2025) Extracellular adenosine deamination primes tip organizer development in *Dictyostelium*. *eLife*, 14.

Zhuang Y, et al. (2025) The LACCASE3/5/12/13 clade mediates seed coat lignin deposition and regulates imbibition and germination. *Cell reports*, 44(12), 116584.